T19.

- CCACTTCCTC GCGAAGGATG CGCTTCCTAC GGTGAAGGAG CAAACTGGTC TCTACGTTCC AGATGCAAGG GTTTGACCAG CGACACCCTT GGAGGGTGC GCGTGCTTGA GTCGGTTGCT AAAGACTATC TAAAAACCCT TTTCTGATAG ATTTTTGGGA CGCACGAACT CAGCCAACGA GCTGTGGGAA CCTCTCCACG
- CCATGGCCCG GCAATCCCTT GAGACCCCTG TCTCGCGGGG CCGCGGGACT ACCGGCTCCG TCCCACGCTG GGTCCTGGGT CCTGCCGCAG CCCTTGGTAT GGTACCGGGC GGGAACCATA GGACGGCGTC CCAGGACCCA AGGGTGCGAC TGGCCGAGGC GGCCGCCTGA CTCTGGGGAC AGAGCGCCCC CGTTAGGGAA 101
- IleProLys ThrLeuLysP heValValVa lIleValAla ValLeuLeuP roValLeuAl aTyrSerAla ThrThrAlaA rgGlnGluGl uValProGln AGTTCCCCAG GICCIGCIGC CAGICCIAGC TIACICIGCC ACCACIGCCC GGCAGGAGGA CCGTCCTCCT CAGGACGACG GTCAGGATCG AATGAGACGG TGGTGACGGG TCGTCGTCGT CATCGTCGCG GTAGCAGCGC AGCAGCAGCA ACCCTAAAGT TGGGATTTCA GATCCCCAAG CTAGGGGTTC 201
- GInThrvala laproGlnGl nGlnArgHis SerPheLysG lyGluGluCy sProAlaGly SerHisArgS erGluHisTh rGlyAlaCys AsnProCysThi GGGAGGAGTG TCCAGCAGGA TCTCATAGAT CAGAACATAC TGGAGCCTGT AACCCGTGCA ACCTCGGACA CCCTCCTCAC AGGICGICCI AGAGIAICIA GICITGIAIG CCCCACAGCA ACAGAGGCAC AGCTTCAAGG TGTCTCCGTG TCGAAGTTCC GGGTGTCGT CAGACAGTGG GTCTGTCACC 301 37
- rCysThrMet CATAAAAGTT CCTGCACCAT GGACGTGGTA GTATTTTCAA GluGlyVa lAspTyrThr AsnAlaSerA snAsnGluPr oSerCysPhe ProCysThrV alCysLysSe rAspGlnLys HisLysSerS CAGAGGGTGT GGATTACACC AACGCTTCCA ACAATGAACC TTCTTGCTTC CCATGTACAG TTTGTAAATC AGATCAAAAA TGTTACTTGG AAGAACGAAG GGTACATGTC AAACATTTAG TCTAGTTTTT TTGCGAAGGT CCTAATGTGG GTCTCCCACA 401 71
 - ACCCCTTCAG rGlyGluVal TGGGGAAGTC uGlyThrPhe ArgAsnGluA snSerProGl uMetCysArg LysCysSerA rgCysProSe GGTGCCCTAG CCACGGGATC GATGTGCCGG AAGTGTAGCA TTCACATCGT CTACACGGCC CGGAATGAAA ACTCCCCAGA GCCTTACTTT TGAGGGGTCT AGGCACCTTC TCCGTGGAAG AGTGTAAAGA TCACATTTCT Thrargasp ThrvalCysG lnCysLysGl GACCAGAGAC ACAGTGTGTC TGTCACACAG CTGGTCTCTG 501

104

- GlnValSerA snCysThrSe rTrpAspAsp IleGlnCysV alGluGluPh eGlyAlaAsn AlaThrValG luThrProAl aAlaGluGlu ThrMetAsnThr TGTTACTTGT ACGACTTCTC TGCTGAAGAG TTTGGGGTCG CTGGGATGAT ATCCAGTGTG TTGAAGAATT TGGTGCCAAT GCCACTGTGG AAACCCCAGC CGGTGACACC TAGGICACAC AACTICTTAA ACCACGGITA GACCCTACTA CAAGICAGIA ATIGIACGIC TAACATGCAG GTTCAGTCAT 137 601
- yThrProAla ProAlaAlaG luGluThrMe tAsnThrSer ProGlyThrP roAlaProAl aAlaGluGlu ThrMetThrT hrSerProGlý GGTCGGGCCC CCAGCCCGGG CCAGCTGCTG AAGAGACAAT GAACACCAGC CCAGGGACTC CTGCCCCAGC TGCTGAAGAG ACAATGACCA TGTTACTGGT ACGACTTCTC GACGGGGTCG GGTCCCTGAG CTTGTGGTCG TTCTCTGTTA GGTCGACGAC GACTCCTGCC CTGAGGACGG CCAGCCGGG GGTCGGGCCC SerProGl 701 171
- CTGAGGACGG YThrProAla CCAGCCCGGG tThrThrSer ProGlyThrP roAlaProAl aAlaGluGlu ThrMetThrT hrSerProGl GGTCGGGCCC AAGAGACAAT GACCACCAGC CCGGGGACTC CTGCCCCAGC TGCTGAAGAG ACAATGACCA TGTTACTGGT GGCCCCTGAG GACGGGTCG ACGACTTCTC CTGGTGGTCG ProAlaAlaG luGluThrMe TICICIGITA CCAGCTGCTG GGTCGACGAC GACTCCTGCC ThrProAla CTGAGGACGG 801 204
- AAATTCCTTC CITICIGAAG IGACACCIIC GAAAGACTTC ACTGTGGAAG CACAAACAAA TICIAATIGI GCTICIGATI GIGITIGITI alLeuIleVa lLeuLeuIle ValPheVal CGAAGACTAA AAGATTAACA GGGATCATAG CCCTAGTATC GlyllelleV GTGGTAGCAT sThrileVal CACCATCGTA TGGAGAGTAC yrLeuSerCy ACCTCTCATG TCTTCTCATT SerSerHisT 901 237
- TCTGCTGTGT TCCCACAGAC AGAAACGCCT AGACGACACA AGGGTGTCTG GGACGGAGGG CACTCTCTGC CCTGCCTCCC GTGAGAGACG GGGCGCTGGA CCCGCGACCT TGAGGGCGGG ACTCCCGCCC AGGCGCTGGC TCCGCGACCG AGGTTCAGGT TCCAAGTCCA CTTACCTGAA SAATGGACTT 1001
- AAAAAAAAA TTTTTTTTT AAAAAAAAA AAAAAAAAA AAAAAAAAA AAAAAAAAA TTTTTTTT AAAAAAAA CAAAAAAAA GTTTTTTTT GCCCCTGCCC 1101

- MetGlnGl yValLysGlu ArgPh LeuPro CGCTTCCTAC GCGAAGGATG GCTGTGGGAA CCTCTCCACG CGCACGAACT CAGCCAACGA TTTCTGATAG ATTTTTGGGA GTTTGACCAG AGATGCAAGG GGTGAAGGAG CCACTTCCTC CGACACCCTT GGAGAGGIGC GCGIGCTIGA GICGGIIGCT AAAGACTAIC TAAAAACCCI CAAACIGGIC ICTACGIICC -
- GGTACCGGGC CCATGGCCCG GGGAACCATA CCCTTGGTAT GGACGCCGTC CCTGCCGCAG TGGCCGAGGC AGGGTGCGAC CCAGGACCCA GGTCCTGGGT TCCCACGCTG ACCGGCTCCG CCGGCGGACT GGCCGCCTGA CTCTGGGGAC AGAGCGCCCC TCTCGCGGGG GAGACCCCTG CGTTAGGGAA GCAATCCCTT 101
 - rgProProAs pGlyArgGly ArgValArgP roArgThrGl nAspGlyVal GlyAsnHisT hrMetAlaArg AGTTCCCCAG GICCIGCIGC CAGICCIAGC ITACICIGCC ACCACIGCCC GGCAGGAGGA CCGTCCTCCT GICAGGAICG AATGAGACGG IGGIGACGGG CAGGACGACG GTAGCAGCGC ACCCTAAAGT TCGTCGTCGT CATCGTCGCG nSerGlyAsp ArgAlaProA AGCAGCAGCA TGGGATTTCA L uGlyAs GATCCCCAAG CTAGGGGTTC 201 -30

IleproLys ThrLeuLysP hevalvalva lilevalAla valLeuLeuP rovalLeuAl aTyrSerAla ThrThrAlaA rgGlnGluGl

- GlnThrvala laproglngl nglnArgHis SerPheLysG lyGluGluCy sProAlaGly SerHisArgS erGluHisTh rGlyAlaCys AsnProCysThr CAGACAGTGG CCCCACAGCA ACAGAGGCAC AGCTTCAAGG GGGAGGAGTG TCCAGCAGGA TCTCATAGAT CAGAACATAC TGGAGCCTGT AACCCGTGCA ACCTCGGACA GTCTTGTATG CCCTCCTCAC AGGTCGTCCT AGAGTATCTA TCGAAGTTCC GGGGTGTCGT TGTCTCCGTG GTCTGTCACC 301 37
- erCysThrMet Gluglyva lAspTyrThr AsnAlaSerA snAsnGluPr oSerCysPhe ProCysThrv alCysLysSe rAspGlnLys HisLysSerS CATAAAAGTT GTATTTTCAA ACAATGAACC ITCITGCITC CCATGTACAG ITTGTAAATC AGATCAAAAA CCIAAIGIGG IIGCGAAGGI IGIIACIIGG AAGAACGAAG GGIACAIGIC AAACAIIIAG ICIAGIIIII CAGAGGGTGT GGATTACACC AACGCTTCCA GTCTCCCACA 401 71
- ACCCCTTCAG GGTGCCCTAG TGGGGAAGTC ThrValCysG lnCysLysGl uGlyThrPhe ArgAsnGluA snSerProGl uMetCysArg LysCysSerA rgCysProSe rGlyGluVal CCACGGGATC TTCACATCGT GACCAGAGAC ACAGTGTC AGTGTAAAGA AGGCACCTTC CGGAATGAAA ACTCCCCAGA GATGTGCCGG AAGTGTAGCA CTACACGGCC TGAGGGGTCT GCCTTACTTT TCCGTGGAAG TGTCACACAG TCACATTTCT Thrargasp CICCICIC 501 104
- GlnValSerA snCysThrSe rTrpAspAsp IleGlnCysV alGluGluPh eGlyAlaAsn AlaThrValG luThrProAl aAlaGluGlu ThrMetAsnThr CIGGGATGAT ATCCAGTGTG ITGAAGAATT TGGTGCCAAT GCCACTGTGG AAACCCCAGC TGCTGAAGAG ACAATGAACA ACGACTTCTC TTTGGGGTCG TAGGICACAC AACITCITAA ACCACGGITA CGGIGACACC GACCCTACTA CAAGICAGIA AITGIACGIC TAACATGCAG GITCAGICAT 601 137
- hrSerProGly GGTCGGGCCC CCAGCCCGGG CCAGCCCGGG GACTCCTGCC CCAGCTGCTG AAGAGACAAT GAACACCAGC CCAGGGACTC CTGCCCCAGC TGCTGAAGAG ACAATGACCA TGTTACTGGT yThrProAla ProAlaAlaG luGluThrMe tAsnThrSer ProGlyThrP roAlaProAl aAlaGluGlu ThrMetThrT GACGGGTCG ACGACTTCTC GGTCCCTGAG CTTGTGGTCG TTCTCTGTTA GGTCGACGAC CTGAGGACGG SerProGl CGTCGGGCCC 701 171
- GACTCCTGCC CTGAGGACGG yThrProAla ProAlaAlaG luGluThrMe tThrThrSer ProGlyThrP roAlaProAl aAlaGluGlu ThrMetThrT hrSerProGl CCAGCCCGGG GGTCGGGCCC CCAGCTGCTG AAGAGACAAT GACCACCAGC CCGGGGACTC CTGCCCCAGC TGCTGAAGAG ACAATGACCA TGTTACTGGT GGCCCCTGAG GACGGGGTCG ACGACTTCTC CIGGIGGICG TICTCIGITA GGTCGACGAC ThrProAla GACTCCTGCC CTGAGGACGG 801 204
- GAAAGACTIC ACTGTGGAAG AAATTCCTTC TGACACCTTC CTTTCTGAAG TCTTCTCAIT ACCTCTCAIG CACCAICGIA GGGAICAIAG IICTAAITGI GCTICTGAIT GIGITIGITI CACAAACAAA SerSerHisT yrLeuSerCy sThrIleVal GlyIleIleV alLeuIleVa lLeuLeuIle ValPheVal CGAAGACTAA CCCTAGTATC AAGATTAACA GTGGTAGCAT AGAAGAGTAA TGGAGAGTAC 901 237
- SAATGGACTT TCCAAGTCCA TCCGCGACCG ACTCCCGCCC CCCGCGACCT GTGAGAGGGG GGACGGAGGG AGACGACACA AGGGTGTCTG TCTTTGCGGA 1101

CITACCIGAA AGGITCAGGI AGGCGCIGGC IGAGGGCGGG GGGCGCIGGA CACICICIGC CCIGCCICCC ICIGCIGIGI ICCCACAGAC AGAAACGCCI

1001

Apo2	1	EQRGQN PRASGARKEHGPGPREARCE RPGLRVPKTL
Apo2DcR	1	ARIPKTLKFV
DR4	51	GRGALPTSI AGPSARER GRAPGPEPAREASPRLAVHKTFKFVVVG
		.
Apo2	41	VVAAVIILVSAESALITOODLAPOORAAPOOKESSESEGLEPPCHHISED
Apo2DcR	13	VIVAVLEPVIAYSATTARQEEVPOOTVAPOQORHSFKGEECPAGSHRSEH
DR4	101	LQVVPSSAATIKTLHDQSIGTQQWEHSPLGELCPPGSHRSER
		CRD1 —
Apo2	91	GRDCISCKYGODYSTHWNDLLFCERCTRCDSGEVELSPCTTIRNTVCCCE
Apo2DcR	63	TGACNPCTEGVDYTHASNNEPSCFPCTVCKSDQKHKSSCTMTRDTYCOCK
DR4	142	PGACNRCTEGYGYTNASNNLFACLPCTACKSDEEERSPCTTTENTACOCK
		CRD2
Apo2	141	EGTEREEDSPEMCERCRIGCPHGMVKVGDCTPWSDLECVHKE
Apo2DcR	113	EGTFRNENSPEMCRKCSR-CPSGEVOVSNCTSWDDIQCVE-EFGANATVE
DR4	192	PGTFRNONSAEMCRKCSTGCPRGMVKVKDCTPWSDIECVHKE
Apo2		
Apo2DcR	161	TPAAEETMNTSPGTPAPAAEETMNTSPGTPAPAAEETMTTSPGTPAPAAE
DR4		
Apo2	183	SGITIGVTVAAVVITVAVFV
Apo2DcR	211	ETMTTSPGTPAPAAEETMTTSPGTPASSHYLSCTIVGIIVIIVLLIVFV
DR4	234	SENGHNIWVILVVILVVPLILVAV-LIVC
Apo2	203	KSLLWKKVLPYLKGICSGGGDPERVDRSSQRPGAEDNVLNEIVSILQP
DR4	262	CIGSGCGGD KCMDRVCFWRLGLIEGPGAEDNAHNEILSNADSLSTFVS
ũ		
Apo2	253	TOVPEGENEVGEPAEPTGVNMLSPGESEHLLEPAEAERSORRELLVPANE
DR4	312	EQOMESQEPADLTGYTVQSPGEAQCLLGPAEAEGSQRRRLLVPANG
W.		
Apo2	303	GDPTETIROCEDDFADIVPFDSWEPIMRKIGIMDNEIKVAKAEAAGHH
DR4	358	ADPTETIMLFFDKFANIVPFDSWDQLMRQLDLTKNEIDVVRAGTAGPG
Apo3/DR3	338	VMDAVPARRWKEFVRTLGLREAKIEAVEVEI-GRF-R VVENVPPLRWKEFVRRLGLSDHEIDRLELQN-GRCLR
TNFR1	322	
CD95	220	iagvhtlsqvægfvækngvneakideikndm-vqdta
4		
Apo2	351	DTLYTMLIKÁVNKTGE-DASVELLDALETIGERLAKOK LEDHLLSSGKE
DR4	406	DALYAMIMKWYNKTGE-NASIETILDALERMEERHAKEKIODLLVDSGKE
Apo3/DR3	374	DOOYEMIKRWRQQQPAGLGAVYAALERMGLDGCVEDLRS
TNFR1	358	EAOYSMLATWRRRTPRREATLELLGRVLRDMDLLGCLEDIEE
CD95	256	ENKVQILRNMHQLHEKKEAY-DÜLKDEKKANLCTLAEKEQT
3	400	AGENTA DESET ST
Apo2		MYLEGNADSALS
DR4	455	IVLEDGTGSAVSLE

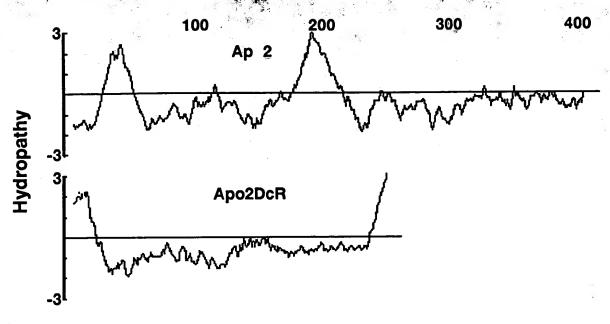


Figure 3

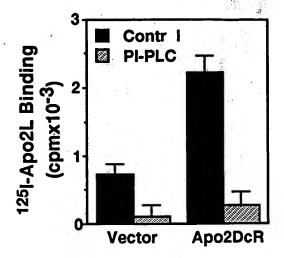


Figure 4

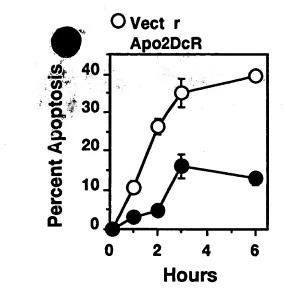
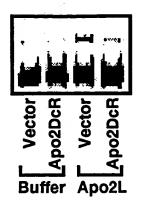


Figure 5



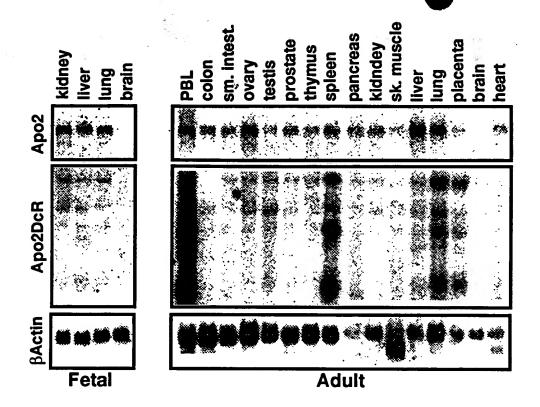


Figure 7

į.

1 CCCACGCGTC CGCATAAATC AGCACGCGGC CGGAGAACCC CGCAATCTCT GCGCCCACAA AATACACCGA CGATGCCCGA TCTACTTTAA GGGCTGAAAC	GGGTGCGCAG GCGTATTTAG TCGTGCGCCG GCCTCTTGGG GCGTTAGAGA CGCGGGTGTT TTATGTGGCT GCTACGGGCT AGATGAAATT CCCGACTTTG
AATACACCGA CGAT	TTATGTGGCT GCTA
r GCGCCCACAA	A CGCGGGTGTT :
CGCAATCTCT	GCGTTAGAGA
CGGAGAACCC	GCCTCTTGGG
AGCACGCGGC	TCGTGCGCCG
CGCATAAATC	GCGTATTAG
1 CCCACGCGTC	GGGTGCGCAG

U	Ų	Gly
CACGGCCCA	GTGCCGGGT	HisGlyPro
CCGGAAAAGG	GGCCTTTTCC	aArgLysArg
CTTCGGGGGC	GAAGCCCCCG	laSerGlyAl
9009900009	၁၅၅၁၁၅၅၅၁	AlaProAlaA
GGGACAGAAC	CCCTGTCTTG	gGlyGlnAsn
TGGAACAACG	ACCTIGITGC	M etGluGlnAr gGlyGlnAsn AlaProAlaA laSerGlyAl aArgLysArg HisGlyProGly
CCTACCGCCA	GGATGGCGGT	Σ
AAGAGCGTTC	TTCTCGCAAG	
GAGAGACTAT	CTCTCTGATA	
101 CCACGGGCCT GAGAGACTAT AAGAGGGTTC CCTACCGCCA TGGAACAACG GGGACAGAAC GCCCCGGCCG CTTCGGGGGC CCGGAAAAGG CACGGCCCAG	GGTGCCCGGA CICTCTGATA TICTCGCAAG GGATGGCGGT ACCTTGTTGC CCCTGTCTTG CGGGCCGGC GAAGCCCCCG GGCCTTTTCC GTGCCGGGTC	
101	•	-1

		.1	
	ZVI GACCCAGGGA GGCGCGGGGA GCCAGGCCTG GGCTCCGGGT CCCCAAGACC CTTGTGCTCG TTGTCGCCGC GGTCCTGCTG TTGGTCTCAG CTGAGTCTG	CTGGGTCCCT CCGCGCCCCT CGGTCCGGAC CCGAGGCCCA GGGGTTCTGG GAACACGAGC AACAGGGGG CCAGGACGAC AACAGGACGAC CAGGACGACGACGACGACGACGACGACGACGACGACGACG	22 ProArgGl uAlaArgGly AlaArgProG lyLeuArgVa lProLvsThr LeuValleuV alvalaal avalleuIeu Ieuvaleera legineeral
	TIGGICTCAG	し上げるじないしてる	TenValsera
	GGTCCTGCTG	CCAGGACGAC	aValT.euT.eu
	TTGTCGCCGC	AACAGCGGCG	alvalalaal
	CTTGTGCTCG	GAACACGAGC	LeuValLeuV
	CCCCAAGACC	GGGGTTCTGG	lProLvsThr
	GGCTCCGGGT	CCGAGGCCCA	lyLeuArqVa
	GCCAGGCCTG	CGGTCCGGAC	AlaArqProG
	GCCCCCCCCCA	CCCCCCCT	uAlaArgGly
	GACCCAGGGA	CIGGGICCCI	ProArgGl
5	TOF		22

ATC	TAG	Ile
ACACCAT	TGTGGTA	VHisHis
301 TCTGATCACC CAACAAGACC TAGCTCCCCA GCAGAGAGCG GCCCCACAAC AAAAGAGGTC CAGCCCCTCA GAGGGATTGT GTCCACCTGG ACACCATATC	AGACTAGTGG GITGITCIGG ATCGAGGGGI CGICTCICGC CGGGGTGITG TITTCICCAG GTCGGGGAGI CICCCTAACA CAGGIGGACC IGIGGIAIAG	55 LeulleThr GinglnAspL euAlaProGl nGlnArgAla AlaProGinG inLysArgSe rSerProSer GluGlyLeuC ysProProGl yHisHisIle
GAGGGATTGT	CICCCIAACA	GluGlyLeuc
CAGCCCCTCA	GTCGGGGAGT	rSerProSer
AAAAGAGGTC	TTTTCTCCAG	lnLysArgSe
GCCCCACAAC	CGGGGTGTTG	AlaProGlnG
GCAGAGAGCG	CGTCTCTCGC	nGlnArgAla
TAGCTCCCCA	ATCGAGGGGT	euAlaProGl
CAACAAGACC	GTTGTTCTGG	GluGlnAspL
TCTGATCACC	AGACTAGTGG	Leullerhr
30T	1	22

401 TCAGAAGACG GTAGAGATTG CATCTCCTGC AAATATGGAC AGGACTATAG CACTCACTGG AATGACCTCC TTTTCTGCTT GCGCTGCACC AGGTGAGTT	AGTOTTOTGC CATOTOTAAC GIAGAGGACG TITATACOTG TOCTGATATO GIGAGTGACC TIACTGGAGG AAAAGACGAA CGCGACGTGG TOCACACTAA	88 SerGluAspG lyArgAspCy sileSerCys LysTyrGlyG lnAspTyrSe rThrHisTrp AsnAspLeuL euPheCysLe uArgCysThr ArgCysAspSer
GCGCTGCACC	CGCGACGTGG	uArgCysThr
TTTTCTCCTT	AAAAGACGAA	euPheCysLe
AATGACCTCC	TTACTGGAGG	AsnAspLeuL
CACTCACTGG	GTGAGTGACC	rThrHisTrp
AGGACTATAG	TCCTGATATC	lnAspTyrSe
AAATATGGAC	TTTATACCTG	LysTyrGlyG
CATCTCCTGC	GTAGAGGACG	sIleSerCys
GTAGAGATTG	CATCTCTAAC	lyargaspCy
TCAGAAGACG	AGTCTTCTGC	SerGluAspG
40T	•	χ χ

ç	ָ יי)ra
CTCC	ייייייייייייייייייייייייייייייייייייייי	tCVS
AGAT	A TOT	luMe
SEC	י אַ ט	rog
TCTC	0 A C A	SerP
GAT	CTA	ASp
AAGAZ	PTCT	luglu
CCCC.	SCCC	Argg
T.I.	AA G	Ph e
CACC	GTGG	yThr
AAGG	TICC	lugl
SAAG	CTTC	31uG
GTGC	CACG	nCys(
T CA	A GT	s Gl
TGTG	ACAC	alcy,
CACAG	STGTC	Thr
AAA (TTT (gAs
CCAG	GGTC	hrar
CGA	GCT	hrT
ACCA	TGGT	Thr
CTGC	SGACG	rocys
ST CC	SASS	r Pı
CTAA(SATT	Ceuse
GGAG	CCTC	lGlu
AGT	GTCCACTTCA CCTCGATTCA GGGACGTGGT GCTGGTCTTT GTGTCACACA GTCACGCTTC TTCCGTGGAA GGCCCTTCTT CTAAGAGGAC TCTTAACACGGC	.uVa
GTGA	CACI	ilygi
501 CAGGTGAAGT GGAGCTAAGT CCCTGCACCA CGACCAGAAA CACAGTGTGT CAGTGCGAAG AAGGCACCTT CCGGGAAGAA GATTCTCCTG AGATGTGCG	GI	122 GlyGluVa lGluLeuSer ProCysThrT hrThrArgAs nThrValCys GlnCysGluG luGlyThrPh eArgGluGlu AspSerProG luMetCysArg
20		12

STATES TABLES	GTAGTAGTAT	
601 GAAGTGCCGC ACAGGGTGTC CCAGAGGGAT GGTCAAGGTC GGTGATTGTA CACCCTGGAG TGACATCGAA TGTGTCCACA AAGAATCAGG CATCATCATA	CTICACGGCG IGICCCACAG GGICTCCCIA CCAGITCCAG CCACIAACAI GIGGGACCIC ACIGIAGCII ACACAGGIGI IICIIAGICC GIAGIAII	
TGTGTCCACA	ACACAGGTGT	
TGACATCGAA	ACTGTAGCTT	
CACCCTGGAG	GTGGGACCTC	
GGTGATTGTA	CCACTAACAT	
GGTCAAGGTC	CCAGTTCCAG	
CCAGAGGGAT	GGTCTCCCTA	
ACAGGGTGTC	TGTCCCACAG	
GAAGTGCCGC	CITCACGGCG IGICCCACAG GGICTCCCIA CCA	
109	i i	

		•
GTAGTAGTAT	yileileile	jū
TICILIAGICC	ysGluSerGl	
ACACAGGIGI	CysValHisL	
THE TRANSPORT OF THE CONTRACT CONCINENCE OF THE PROPERTY OF THE PROPERTY ACACAGOIGI TICITIAGING CITAGINAL	TrpSe rAspIleGlu CysValHisL ysGluSerGl yIlellelle	
してしてもりりてり	hrProTrpSe	
てなりななべりなりり	alLysVal GlyAspCysT hrProTrpSe	
0000110000	tValLysVal	
5100010100	roArgGlyMe	
	ThrGlyCysP	
	LysCysArg ThrGlyCysP roArgGlyMe tVall	
1	155	

	,	
101 GGAGTCACAG TIGCAGCCGI AGICITGAIT GIGGCIGIGI ITGITIGCAA GICITIACIG IGGAAGAAAG ICCITCCIIA CCIGAAAGGC AICIGCIGAG	CCTCAGTGTC AACGTCGGCA TCAGAACTAA CACCGACACA AACAAACGTT CAGAAATGAC ACCTTCTTTC AGGAAGGAAT GGACTTTCCG TAGACGAGTC	188 GlyValThrV alAlaAlaVa lValLeuile ValAlaValP heValCysLy sSerLeuLeu TrpLysLysV alLeuProTy rLeuLysGly ileCysSerGly
CCTGAAAGGC	GGACTTTCCG	rLeuLysGly
TCCTTCCTTA	AGGAAGGAAT	alLeuProTy
TGGAAGAAAG	ACCTTCTTTC	TrpLysLysV
GTCTTTACTG	CAGAAATGAC	sSerLeuLeu
TIGITICCAA	AACAAACGTT	heValCysLy
GTGGCTGTGT	CACCGACACA	ValAlaValP
AGTCTTGATT	TCAGAACTAA	lValLeuIle
TIGCAGCCGI	AACGTCGGCA	alAlaAlaVa
GGAGTCACAG	CCTCAGTGTC	GlyvalThrv
/01	•	188

GlyGlyGl yAspProGlu ArgValAspA rgSerSerGl nArgProGly AlaGluAspA snValLeuAs nGluIleVal SerIleLeuG lnProThrGln AGCCCACCCA TCGGGTGGGT 801 GTGGTGGTGG GGACCCTGAG CGTGTGGACA GAAGCTCACA ACGACCTGGG GCTGAGGACA ATGTCCTCAA TGAGATCGTG AGTATCTTGC TCATAGAACG TACAGGAGTT ACTCTAGCAC GCACACCTGT CTTCGAGTGT TGCTGGACCC CGACTCCTGT CCTGGGACTC CACCACCACC 222

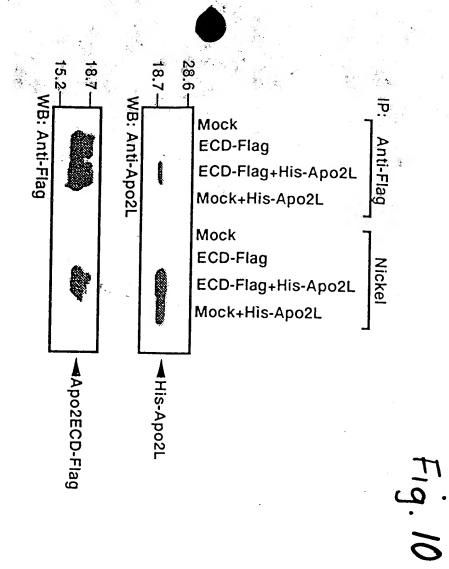
TAGACGACCT TGGCCGTCTT CAGGAAATGG AAGTCCAGGA GCCAGCAGAG CCAACAGGTG TCAACATGTT GTCCCCGGG GAGTCAGAGC ATCTGCTGGA ACCGGCAGAA ValProGlu GlnGluMetG luValGlnGl uProAlaGlu ProThrGlyV alAsnMetLe uSerProGly GluSerGluH isLeuLeuGl uProAlaGlu GGTTGTCCAC AGTTGTACAA CAGGGGGCCC CTCAGTCTCG CGGTCGTCTC TTCAGGTCCT GTCCTTTACC GGTCCCTGAG CCAGGGACTC 901 255

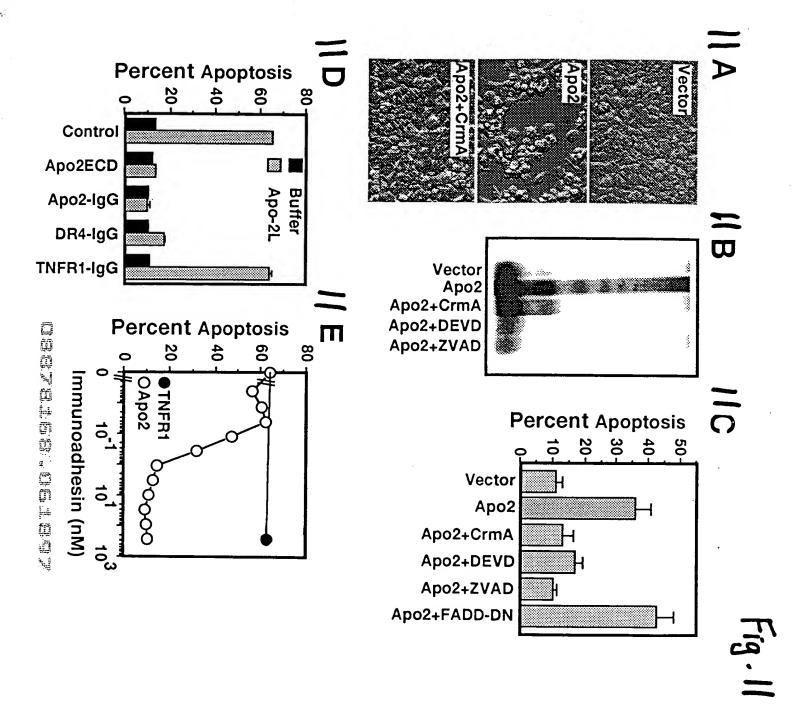
²⁸⁸ AlaGluArgS erGlnArgAr gArgLeuLeu ValProAlaA snGluGlyAs pProThrGlu ThrLeuArgG lnCysPheAs pAspPheAla AspLeuValPro 1001 GCTGAAAGGT CTCAGAGGAG GAGGCTGCTG GTTCCAGCAA ATGAAGGTGA TCCCACTGAG ACTCTGAGAC AGTGCTTCGA TGACTTTGCA GACTTGGTGC CGACTITCCA GAGICTCCIC CICCGACGAC CAAGGICGII TACITCCACI AGGGIGACIC IGAGACICIG ICACGAAGCI ACIGAAACGI CIGAACCACG

		-		÷		
ACTIGGCCT TO A TO A TOTAL AND THE STATE OF TOOCTANGE TO TOOCTOCG GOCCACAGG ACACCTIGIA TO A A TOOLT TO A CONTROL ACTICGACAGA GOOCT TO TOTACACCCGA GOOCT TO TOTACACAGA GOOCT TO TOTACACAGA ACTICGACAGA CONTROL A TOTACAGA ACTICGACAGA CONTROLA A TOTACAGA A TOTACAGA SPINILE TAY A SECULLAR A CONTROLA A TOTACAGA A TOTACAGA A TOTACAGA A SPINILE TAY A SECULLAR A CONTROLA A SPINILE AND A SP	TGCCAAGCAG ACGTTCGTC uAlaLysGln	GGAAGTGAGA CCTTCACTCT	AGAAACTCTC TCTTTGAGAG	CTATGGAAAT	ATTTÄTTTAT TAAATAAATA	GCCATGGCC CGGTACCGG
GGCCACAGGG CCGGTGTCCC GlyHisArgA	GAGAGAGACT CTCTCTGA lyGluArgLe	ATTCTCTTCA TAAGAGAAGT	CGGTACTGGA GCCATGACCT	AATAAGGACA TTATTCCTGT	TATCCTAATG TAAATGCTTT ATAGGATTAC ATTTACGAAA	AAGCTTGGCC TTCGAACCGG
TGAGGCAGCG ACTCCGTCGC aGluAlaAla	GAGACGCTGG CTCTGCGACC GluThrLeuG	CCTAAGTGTG GGATTCACAC erOC*	GTCACATGAC	TGAATGTGAT ACTTACACTA	TATCCTAATG ATAGGATTAC	CGACCTGCAG GCTGGACGTC
TGGCTAAAGC ACCGATTTCG alalaLysAl	GGATGCCTTG GAGACGCTGG GAGAGAGACT TGCCAAGCAG CCTACGGAAC CTCTCTCTGA ACGGTTCGTC UASPAlaLeu GluThrLeuG lyGluArgLe uAlaLysGln	TAATGCAGAC TCTGCCWTGT CCTAAGTGTG ATTCTCTTCA GGAAGTGAGA ATTACGTCTG AGACGGAACA GGATTCACAC TAAGAGAAGT CCTTCACTCT YASNAlaAsp SeralaXqqS eroC*	TGCCACAATT GTCACATGAC CGGTACTGGA AGAAACTCTC ACGGTGTTAA CAGTGTACTG GCCATGACCT TCTTTGAGAG	TTTTATAAGC AAAATATTCG	AGCACTTTTT TCGTGAAAAA	ACTCTAGAGT TGAGATCTCA
CTGGGAGCCG CTCATGAGGA AGTTGGGCCTTCTATTGAGATARAGG TGCCTAAAGC TGAGGCAGCG GGCCACAGGG ACACCTTGTA GACCTCGGG CTCAGGG ACACCTTGTA GACCTCGGC GACCTCGC GGCCACAGGG ACACCTCGGC GACCCTCGGC GACCTCGC TGTGGAACAT ATTAGIUPTO Leumetargi ysleuGlyle umetaspasn Gluilelysv alalalysal aGlualaala GlyHisarga spThrieuTy	GCCTCTGTCC ACACCCTGCT GGATGCCTTG GAGACGCTGG GAGAGAGACT TGCCAAGCAG CGGAGACAGG TGTGGGACGA CCTACGGAAC CTCTGCGACC CTCTCTCTA ACGGTTCGTC AlaserValH isThrLeuLe uAspAlaLeu GluThrLeuG lyGluArgLe uAlaLysGln	ATCTAGAAGG TAATGCAGAC TCTGCCWTGT CCTAAGTGTG ATTCTCTTCA GGAAGTGAGA TAGATCTTCC ATTACGTCTG AGACGGAACA GGATTCACAC TAAGAGAAGT CCTTCACTCT YrLeuGluGl yAsnAlaAsp SerAlaXqqS erOC*	AGTAGGAAAG TCATCCTTTC	TTCACTGCAC TIGGCATTAT TITTATAAGC TGAATGTGAT AATAAGGACA CTATGGAAAT AAGTGACGTG AACCGTAATA AAAATATTCG ACTTACACTA TTATTCCTGT GATACCTTTA	TGGGATGTCA TTGTTTTCAC AGCACTTTTT ACCCTACAGT AACAAAAGTG TCGTGAAAAA	GGCGGCCGCG ACTCTAGAGT CGACCTGCAG AAGCTTGGCC GCCATGGCC CCGCCGGCGC TGAGATCTCA GCTGGACGTC TTCGAACCGG CGGTACCGG
CATGACAAT CACCTGTTA UMETASPASN	GCCTCTGTCC CGGAGACAGG AlaSerValH	ATCTAGAAGG TAGATCTTCC YrLeuGluGl	GACTCCAGTC CTGAGGTCAG		TGGGATGTCA ACCCTACAGT	AAAAAAAAG TTTTTTTTC
AGTTGGGCGT. TCAACCCGGA YSLeuGlyLe	CGGGCGAGAT GCCCGCTCTA rGlyArgAsp	AAGATTGAGG ACCACTTGTT GAGCTCTGGA AAGTTCATGT TTCTAACTCC TGGTGAACAA CTCGAGACCT TTCAAGTACA LyslleGluA spHisLeuLe uSerSerGly LysPheMetT	AGCCCAACTG TCGGGTTGAC	TCACCCAGTG GATGGAACAT CCTGTAACTT AGTGGGTCAC CTACCTTGTA GGACATTGAA	AGATTTGGTT TCTAAACCAA	AAAAAAAAA TTTTTTTT
CTGGGAGCCG CTCATGAGGA GACCCTCGGC GAGTACTCCT rTrpGluPro LeuMetArgL	TCAACAAAAC AGTTGTTTTG alasnLysTh	GAGCTCTGGA CTCGAGACCT uSerSerGly	TTCTGGAAAA AAGACCTTTT	GATGGAACAT CTACCTTGTA	GCGTACTTTG CGCATGAAAC	CATCTACAAA GTAGATGTTT
CTGGGAGCCG GACCCTCGGC rTrpGluPro	ATAAAGTGGG TCAACAAAAC TATTTCACCC AGTTGTTTTG IleLysTrpV alAsnLysTh	ACCACTTGTT TGGTGAACAA SPHisLeuLe	TTTACCTTTT TTCTGGAAAA AAATGGAAAA AAGACCTTTT	TCACCCAGTG AGTGGGTCAC	TTCCGTTTGT GCGTACTTTG AAGGCAAACA CGCATGAAAC	TTGTAAGATC AACATTCTAG
1101 CCTTTGACTC CTGGGAGCCG CTCATGAGGA AGTTGGGCTTTTTTTTTT	1201 CACGATGCTG ATAAAGTGGG TCAACAAAAC CGGGCGAGAT GCCTCTGTCC ACACCCTGCT GGATGCCTTG GAGACGCTGG GAGAGAGAT TGCCAAGCAG GTGCTACGAC TATTTCACCC AGTTGTTTTG GCCCGCTCTA CGGAGACAGG TGTGGGACGA CCTACGGAAC CTCTGCGACC CTCTCTTGA ACGGTTCGTC 355 ThrMetLeu IleLysTrpV alasnLysTh rGlyArgasp AlaserValH isThrLeuLe uaspalaLeu GluthrLeuG lyGluargLe ualaLysGln	1301 AAGATTGAGG ACCACTTGTT GAGCTCTGGA AAGTTCATGT TTCTAACTCC TGGTGAACAA CTCGAGACCT TTCAAGTACA 388 LyslleGluA spHisLeuLe uSerSerGly LysPheMetT	1401 CCTTCCCTGG TTTACCTTTT TTCTGGAAAA AGCCCAACTG GACTCCAGTC AGTAGGAAAG TGCCACAATT GTCACATGAC CGGTACTGGA AGAAACTCTC GGAAGGGACC AAATGGAAAA AAGACCTTTT TCGGGTTGAC CTGAGGTCAG TCATCCTTTC ACGGTGTTAA CAGTGTACTG GCCATGACCT TCTTTGAGAG	CCATCCAACA TCACCCAGTG GATGGAACAT CCTGTAACTT GGTAGGTTGT AGTGGGTCAC CTACCTTGTA GGACATTGAA	1601 GICIGGAICA IICCGITIGI GCGIACITIG AGAITIGGII IGGGAIGICA IIGIIIITCAC AGCACITITI IAICCIAAIG IAAAIGCITI AILIAI CÂGACCIAGI AAGGCAAACA CGCAIGAAAC ICIAAACCAA ACCCIACAGI AACAAAAGIG ICGIGAAAAA AIAGGAITAC AITIACGAAA IAAAIAAAIA	1701 TTGGGCTACA TTGTAAGATC CATCTACAAA AAAAAAAAA AAAAAAAAG GGCGGCCGCG ACTCTAGAGT CGACCTGCAG AAGCTTGGCC GCCATGGCC AACCCGATGT AACATTCTAG GTAGATGTTT TTTTTTTTT TTTTTTTC CCGCCGGCGC TGAGATCTCA GCTGGACGTC TTCGAACGG CGGTACCGG
1101	1201	1301	1401	1501	1601	1701
11						

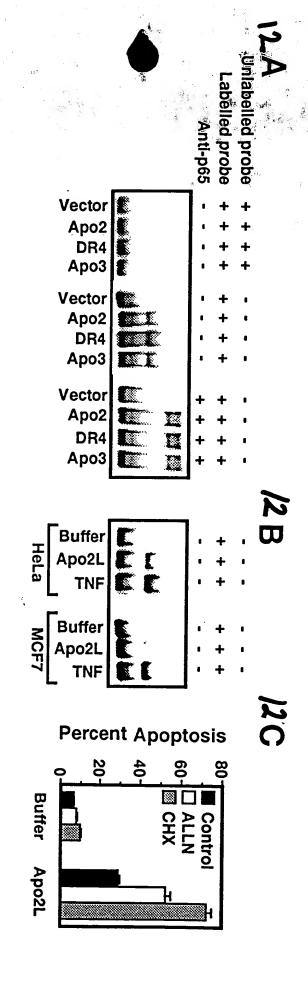
Fig. 8 (cont.)

<u>MEQRGONAPAASGARKRHGPGPREARGARPGLRVPKTLVLVVAAVLLLVSAESALITQQD</u> LAPQQRAAPQQKRSSPSEGLCPPGHHISEDGRDCIS<u>C</u>KYGQDYSTHWNDLLF<u>C</u>LR<u>C</u>TR<u>C</u> SGEVELSPCTTTRNTVCQCEEGTFREEDSPEMCRKCRTGCPRGMVKVGDCTPWSDIECVH NVLNEIVSILQPTQVPEQEMEVQEPAEPTGVNMLSPGESEHLLEPAEAERSQRRRLLVPA KE<mark>SGIIIGVTVAAVVLIVAVFVCKSLLM</mark>KKVLPYLKGICSGGGDPERVDRSSQRPGAED NEGDPTETLRQCFDDFADLVPFDSWEPLMRKLGLMDNEIKVAKAEAAGHRDTLYTMLIKW VNKTGRDASVHTLLDALETLGERLAKOKIEDHLLSSGKFMYLEGNADSALS 241 301 61 181





12



71G. /a



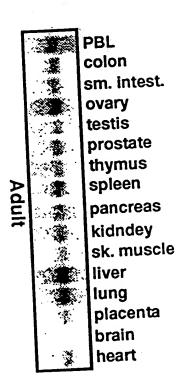


FIG. 13